

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: June 21, 2003, 19:16:44 ; Search time 1433 Seconds
(without alignments)
214.724 Million cell updates/sec

Title: US-09-581-500B-14

Perfect score: 19
Sequence: 1 cgcctcgtatcctcctcctg 19

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbta:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	91.6	522	12	BG347460
2	17.4	91.6	1039	9	AU050798
3	17.4	91.6	1101	17	CNS04VNO
4	17	89.5	187	17	AZ248177
5	17	89.5	250	17	AZ083738
6	17	89.5	772	12	BF627795

C	7	16.4	86.3	256	13	BT293206	BT293206	UT-R-DKO-
	8	16.4	86.3	259	9	AA884860	AA884860	am21b02.s
	9	16.4	86.3	267	12	BF551260	BF551260	UT-R-CO-1
	10	16.4	86.3	292	14	BQ237385	BQ237385	TAE05017F
	11	16.4	86.3	318	17	AZ774858	AZ774858	2M0004J11
	12	16.4	86.3	331	17	BM125791	BM125791	BM125791
	13	16.4	86.3	353	13	BG994801	BG994801	PMO-HT091
	14	16.4	86.3	364	14	T11530	T11530	AT1480P
	15	16.4	86.3	392	12	BF086663	BF086663	CKO-CO07
	16	16.4	86.3	435	9	AA998619	AA998619	UT-R-CO-1
	17	16.4	86.3	465	9	AA998179	AA998179	UT-R-CO-1
	18	16.4	86.3	466	9	AA998179	AA998179	UT-R-CO-1
	19	16.4	86.3	497	12	BF410904	BF410904	UT-R-CO-1
	20	16.4	86.3	499	17	AZ127320	AZ127320	OSUNB008
	21	16.4	86.3	516	10	BE374792	BE374792	60122608
	22	16.4	86.3	525	12	BF190964	BF190964	237645
	23	16.4	86.3	528	9	AA178165	AA178165	EST221830
	24	16.4	86.3	535	10	BT010299	BT010299	UT-R-BU1-
	25	16.4	86.3	538	13	BUT44737	BUT44737	BU244737
	26	16.4	86.3	538	17	AZ644006	AZ644006	IM0507618
	27	16.4	86.3	545	17	AQ041975	AQ041975	CIT-HSP-2
	28	16.4	86.3	554	10	BE100774	BE100774	UT-R-BU1-
	29	16.4	86.3	577	17	AQ870513	AQ870513	nbe000398
	30	16.4	86.3	578	17	AZ483135	AZ483135	IM0308C10
	31	16.4	86.3	591	17	AQ491443	AQ491443	RPC1-11-2
	32	16.4	86.3	616	12	BG162703	BG162703	DEL17d05.Y
	33	16.4	86.3	685	10	BE410269	BE410269	601302549
	34	16.4	86.3	705	14	BQ209524	BQ209524	UT-R-BPO-
	35	16.4	86.3	719	17	AZ484914	AZ484914	2M0150B08
	36	16.4	86.3	720	12	BE729865	BE729865	601562449
	37	16.4	86.3	720	13	BE150819	BE150819	603297714
	38	16.4	86.3	748	12	BG671778	BG671778	DRNEXG12
	39	16.4	86.3	782	13	BI558945	BI558945	603241302
	40	16.4	86.3	831	12	BE876298	BE876298	601486615
	41	16.4	86.3	857	9	AU141539	AU141539	AV141539
	42	16.4	86.3	884	17	AQ742984	AQ742984	HS-5386
	43	16.4	86.3	1003	17	AG110540	AG110540	Pan trogl
	44	16.4	86.3	2307	11	BC021805	BC021805	Hom sapi
	45	16.4	86.3	2586	11	BC007638	BC007638	Hom sapi

ALIGNMENTS

RESULT 1
BG347460
LOCUS
DEFINITION
522 bp mRNA linear EST 28-FEB-2001
dab87a11.x1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4404381
3 similar to SW:NP04_YEAST P37838 NUCLEOLAR PROTEIN NOP4 ; mRNA
SEQUENCE
BG347460
BG347460.1 GI:13167884
VERSION
KEYWORDS
SOURCE
ORGANISM
African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE
1 (bases 1 to 522)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.,
Martin,J., Wyllie,T., Underwood,K., Theising,B., Bowers,Y., Person
B., Gibbons M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterson,R. and Wilson,R.
Washu Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwatson.wustl.edu
Library constructed by Life Technologies. DNA Sequencing by:

Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E.B. Consortium/INLML at: info@image.lml.gov
 Seq primer: -400P from GIBCO
 High quality sequence stop: 433.

FEATURES

Location/Qualifiers

1..522

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="IMAGE:4404381"

/clone_id="NICHD XGC Emb2"

/tissue_type="embryo, stage 17/19"

/lab_host="MD10B (phage-resistant)"

/note="vector: PCWV-SPORT6; Site 1: NotI; Site 2: SalI;

Cloned unidirectionally. Primer: Oligo dT. Average insert

size 2.1 Kb. Constructed by Life Technologies."

BASE COUNT

95 a 150 c 74 g 203 t

ORIGIN

Query Match 91.6%; Score 17.4; DB 12; Length 522;

Best Local Similarity

94.7%; Pred. No. 1.8e+03; Mismatches 1; Indels 0; Gaps 0;

Matches

18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 CGCTCGATTCCTGCTCTG 19

DB

230 CGCTCGATTCCTGCTCTG 248

RESULT 2

LOCUS

A0050798 1039 bp mRNA linear EST 08-JUN-1999

DEFINITION

A0050798 Paralicthys olivaceus library (Aoki T) Paralicthys

ACCESSION

A0050798 Paralicthys olivaceus library (Aoki T) Paralicthys

VERSION

A0050798.1 GI:5019251

KEYWORDS

EST.

SOURCE

Paralicthys olivaceus

ORGANISM

Paralicthys olivaceus

AUTHORS

Aoki, T.

TITLE

Japanese flounder leukocyte cDNA

JOURNAL

Unpublished (1999)

COMMENT

Contact: Takashi Aoki

REFERENCE

Aquatic Biosciences

AUTHORS

Tokyo University of Fisheries

TITLE

Konan 4-5-7, Tokyo, Minato-Ku 108-8477, Japan

JOURNAL

Tel: 81-3-5463-0689

COMMENT

Fax: 81-3-5463-0690

REFERENCE

Email: aoki@tokyo-u-fish.ac.jp

AUTHORS

clone WH1-23: similar to rat nuclear pore complex (U1840).

TITLE

Location/Qualifiers

JOURNAL

1..1039

COMMENT

/organism="Paralicthys olivaceus"

AUTHORS

/db_xref="taxon:8255"

TITLE

/clone="WH1-23"

JOURNAL

/clone_id="Paralicthys olivaceus library (Aoki T)"

COMMENT

/note="Organ: spleen"

REFERENCE

/note="Organ: spleen"

AUTHORS

234 a 282 c 266 g 247 t 10 others

TITLE

Query Match 91.6%; Score 17.4; DB 9; Length 1039;

Best Local Similarity

94.7%; Pred. No. 2.3e+03; Mismatches 1; Indels 0; Gaps 0;

Matches

18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 CGCTCGATTCCTGCTCTG 19

DB

339 CGCTCGATTCCTGCTCTG 357

RESULT 3
 CDS04VNO/c
 LOCUS
 DEFINITION
 Tetraodon nigroviridis genome survey sequence T3 end of clone
 010F19 of library A from tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION

AL309309

VERSION

AL309309.1 GI:8216248

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis.

ORGANISM

Tetraodon nigroviridis

REFERENCE

1 (bases 1 to 1101)

AUTHORS

Roeset-Crollius, H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C.,

TITLE

Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,

JOURNAL

Saurin, W. and Weissenbach, J.

COMMENT

Human gene number estimate provided by genome wide analysis using

REFERENCE

Unpublished

AUTHORS

2 (bases 1 to 1101)

TITLE

Characterization and repeat analysis of the compact genome of the

JOURNAL

freshwater pufferfish Tetraodon nigroviridis

COMMENT

Unpublished

REFERENCE

3 (bases 1 to 1101)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (12-APR-2000)

COMMENT

This sequence is a single read and was generated as part of a large

REFERENCE

scale clone-end sequencing project of the Tetraodon nigroviridis

AUTHORS

genome. For more information, please take a look at

TITLE

http://www.genoscope.cns.fr/Tetraodon.

JOURNAL

Location/Qualifiers

COMMENT

1..1101

REFERENCE

/organism="Tetraodon nigroviridis"

AUTHORS

/db_xref="taxon:99883"

TITLE

/clone="010F19"

JOURNAL

/clone_id="A"

COMMENT

/note="Genoscope sequence ID: COA010CC10A1-end : T3"

REFERENCE

BASE COUNT 253 a 324 c 294 g 211 t 19 others

AUTHORS

Query Match 91.6%; Score 17.4; DB 17; Length 1101;

Best Local Similarity

94.7%; Pred. No. 2.3e+03; Mismatches 1; Indels 0; Gaps 0;

Matches

18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 CGCTCGATTCCTGCTCTG 19

DB

392 CGCTCGATTCCTGCTCTG 374

RESULT 4

AZ248177 187 bp DNA linear GSS 15-JUN-2000

LOCUS

RCPT-23-39M14.TV RCPT-23 Mus musculus genomic clone RCPT-23-39M14,

DEFINITION

DNA sequence.

ACCESSION

AZ248177

VERSION

AZ248177.1 GI:8561380

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

TITLE

1 (bases 1 to 187)

JOURNAL

Zhao, S., Nierman, W., Feldlynn, T., Malek, T., Shatsman, S., Akintet

COMMENT

B., Levins, M., McGann, S., Tsagaye, G., Geer, K., Krol, M., de Jong, P.

REFERENCE

and Fraser, C.M.

AUTHORS

Mouse BAC End Sequences from Library RCPT-23

TITLE

JOURNAL
COMMENT

Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (<http://info@resgen.com>). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 39 row: M column: 14
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1. 187
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-39M14"
/clone_id="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 58 a 30 c 65 g 34 t
ORIGIN

Query Match 89.5%; Score 17; DB 17; Length 187;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCT 18
|||||
Db 27 GCTCTGATTCCTGCTCT 43

RESULT 5
AZ083738 250 bp DNA linear GSS 08-MAY-2000
LOCUS
DEFINITION RPCI-23-22N10.TV RPCI-23 Mus musculus genomic clone RPCI-23-22N10,
DNA sequence.
ACCESSION
AZ083738
VERSION
AZ083738.1 GI:7725471
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 250)
Bao, S., Niernan, W., Feldblum, T., Malek, J., Shatsman, S., Akinrost,
B., Levins, M., Moggan, S., Tesgaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-22N10.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong

FEATURES
source

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (<http://info@resgen.com>). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 22 row: N column: 10
Seq primer: SP6
Class: BAC ends.

Location/Qualifiers
1. 250
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-22N10"
/clone_id="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 71 a 35 c 80 g 64 t
ORIGIN

Query Match 89.5%; Score 17; DB 17; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCT 18
|||||
Db 44 GCTCTGATTCCTGCTCT 60

RESULT 6
BF627795/c 772 bp mRNA linear EST 22-OCT-2001
LOCUS
DEFINITION HVSMB0005N04f Hordeum vulgare seedling shoot EST library
HYCDNA0002 (dehydration stress) Hordeum vulgare cDNA clone
HVSMB0005N04f, mRNA sequence.
ACCESSION
BF627795
VERSION
BF627795.2 GI:13090001
KEYWORDS
EST.
SOURCE
Hordeum vulgare.
ORGANISM
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
Triticeae; Hordeum.

1 (bases 1 to 772)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Fritsch, D., Yu,
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton,
R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored RST resource
for barley genomics: Morex drought-stressed seedling shoot cDNA
library
Unpublished (2001)
On Dec 19, 2000 this sequence version replaced gi:11891953.
Contact: Wing RA
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 131
Seq primer: AATTACCTCCTAAGAGG
High quality sequence stop: 215.
location/Qualifiers
1. 772
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"

FEATURES
source

location/Qualifiers
1. 772
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 259)
AUTHORS NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40m3 fwd. RT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..259
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1467435"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="MDH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH19W, testis NT, and B-cell NC1 CGAP GCBI) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687233, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 50 a 93 c 57 g 59 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 259;
Best Local Similarity 94.4%; Pred. No. 4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCTG 19
DB 42 GCTCTGATTCCTGCTCTG 59

RESULT 9 267 bp mRNA linear EST 12-DEC-2000
LOCUS BF551260
DEFINITION UI-R-C0-19-e-05-0-UI-r1 UI-R-C0 Rattus norvegicus cDNA clone
VERSION BF551260
KEYWORDS BF551260.1 GI:11660990
SOURCE EST.
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 267)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LNL (infoimage.lnl.gov). IMAGE ID= 1774202
Seq primer: M13 Forward.
Location/Qualifiers
1..267
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-19-e-05-0-UI"
/clone_lib="UI-R-C0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)."

BASE COUNT 56 a 82 c 52 g 77 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 267;
Best Local Similarity 94.4%; Pred. No. 4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCTG 19
DB 219 GCTCTGATTCCTGCTCTG 236

RESULT 10 292 bp mRNA linear EST 03-MAY-2002
LOCUS B0237385
DEFINITION TAb05017F05F TAb05 Triticum aestivum cDNA clone TAb05017F05F, mRNA sequence.
VERSION B0237385
KEYWORDS B0237385.1 GI:20433261
SOURCE EST.
ORGANISM bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 292)
AUTHORS Cloutier,S.
TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-Food Canada
195 D'Arce Rd, Winnipeg, MB, Canada R3T 2M5
Tel: (204) 983-2340

Fax: (204) 983-4604
Email: scloutiere@agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 017 row: F column: 05
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
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/organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TA805017P05P"
/clone_1ib="TA805"
/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"
BASE COUNT 50 a 67 c 109 g 66 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 14; Length 292;
Best Local Similarity 94.4%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 2 GCTCTGATTCCTGCTCTG 19
DB 58 GCTCTGATTCCTGCTCTG 75

RESULT 11
A2774858 318 bp DNA linear GSS 16-FEB-2001
LOCUS A2774858
DEFINITION 2M0004J1JR Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUGCM0004J11 R, DNA sequence.
ACCESSION A2774858
VERSION A2774858.1 GI:12900749
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 318)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: J column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 318.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0004J11"
/clone_1ib="Mouse 10kb plasmid UUGCM library"
/sex="Male"

FEATURES

Location/Qualifiers
1..318
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0004J11"
/clone_1ib="Mouse 10kb plasmid UUGCM library"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD2uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gil472114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 86.3%; Score 16.4; DB 17; Length 318;
Best Local Similarity 94.4%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 2 GCTCTGATTCCTGCTCTG 19
DB 70 GCTCTGATTCCTGCTCTG 87

RESULT 12
B125791/c 331 bp mRNA linear EST 28-JUN-2000
LOCUS B125791/c
DEFINITION B125791 RIKEN full-length enriched, 16 days neonate cerebellum Mus
musculus cDNA clone 963008W03 3', mRNA sequence.
ACCESSION B125791
VERSION B125791.1 GI:8780123
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 331)
Komo,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomioka,N., Toya,
T., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yamataka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Komo,H., et al.)
Unpublished (2000)

JOURNAL
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Muramatsu,Y. and Hayashizaki,Y.
Thermozabilization and thermostabilization of thermolabile enzymes by
thermalase and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

ORIGIN

Query Match 86.3%; Score 16.4; DB 14; Length 364;
 Best Local Similarity 94.4%; Pred. No. 4.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGCTCGATTCCTGCTCT 18
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 Db 95 CGCTCGATTCGAGCTCT 112

RESULT 15

BR086663/c 392 bp mRNA linear EST 19-OCT-2000
 LOCUS CM0-GN0079-150900-547-d04 GN0079 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BR086663
 VERSION BR086663.1 GI:10892373
 KEYWORDS
 SOURCE EST.
 ORGANISM human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 392)

REFERENCE
 AUTHORS
 Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Bunnstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.U.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL
 MEDLINE
 COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663

Contact: Simpson A.U.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 http://www.ludwig.org.br/scripts/gethtml2.pl?c1=kt2-CM0-GN0079-150
 900-547-d04&t3=2000-09-15&r4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 39
 High quality sequence stop: 392.
 Location/Qualifiers

FEATURES

source

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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0079"
 /dev_stage="Adult"
 /note="Organ: Placenta, normal; Vector: puc18; Site 1: SmaI
 ; Site 2: SmaI; A mini-library was made by cloning
 products derived from ORS878 PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the pUC 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."

BASE COUNT 91 a 97 c 74 g 130 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 392;
 Best Local Similarity 94.4%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTCTGATTCCTGCTCTG 19
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 Db 39 GGTCTGATTCGAGCTCTG 22

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 19:56:29 ; Search time 121 Seconds
(without alignments)
230.422 Million cell updates/sec

Title: US-09-581-500B-14

Perfect score: 19
Sequence: 1 cgcctcgtactcgtctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCONB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	16.4	86.3	1769	10 US-09-728-952-95
2	16.4	86.3	2550	9 US-10-028-072-59
3	16.4	86.3	2550	9 US-10-121-049-59
4	16.4	86.3	2550	9 US-10-123-045-59
5	16.4	86.3	2550	9 US-10-140-470-59
6	16.4	86.3	2550	9 US-10-175-746-59
7	16.4	86.3	2550	9 US-10-176-918-59
8	16.4	86.3	2550	9 US-10-176-921-59
9	16.4	86.3	2550	9 US-10-137-865-59
10	16.4	86.3	2550	9 US-10-140-474-59
11	16.4	86.3	2550	9 US-10-142-431-59
12	16.4	86.3	2550	9 US-10-143-114-59
13	16.4	86.3	2550	9 US-10-140-002-59
14	16.4	86.3	2550	9 US-10-142-419-59
15	16.4	86.3	2550	9 US-10-123-262-59
16	16.4	86.3	2550	9 US-10-142-423-59
17	16.4	86.3	2550	9 US-10-121-050-59
18	16.4	86.3	2550	9 US-10-141-756-59
19	16.4	86.3	2550	9 US-10-143-032-59

20	16.4	86.3	2550	9 US-10-123-108-59	Sequence 59, Appl
21	16.4	86.3	2550	9 US-10-123-236-59	Sequence 59, Appl
22	16.4	86.3	2550	9 US-10-123-261-59	Sequence 59, Appl
23	16.4	86.3	2550	9 US-10-140-921-59	Sequence 59, Appl
24	16.4	86.3	2550	9 US-10-140-928-59	Sequence 59, Appl
25	16.4	86.3	2550	9 US-10-121-045-59	Sequence 59, Appl
26	16.4	86.3	2550	9 US-10-123-292-59	Sequence 59, Appl
27	16.4	86.3	2550	9 US-10-123-903-59	Sequence 59, Appl
28	16.4	86.3	2550	9 US-10-124-819-59	Sequence 59, Appl
29	16.4	86.3	2550	9 US-10-124-822-59	Sequence 59, Appl
30	16.4	86.3	2550	9 US-10-140-498-59	Sequence 59, Appl
31	16.4	86.3	2550	9 US-10-121-041-59	Sequence 59, Appl
32	16.4	86.3	2550	9 US-10-121-047-59	Sequence 59, Appl
33	16.4	86.3	2550	9 US-10-121-043-59	Sequence 59, Appl
34	16.4	86.3	2550	9 US-10-121-047-59	Sequence 59, Appl
35	16.4	86.3	2550	9 US-10-123-215-59	Sequence 59, Appl
36	16.4	86.3	2550	9 US-10-123-902-59	Sequence 59, Appl
37	16.4	86.3	2550	9 US-10-123-908-59	Sequence 59, Appl
38	16.4	86.3	2550	9 US-10-123-909-59	Sequence 59, Appl
39	16.4	86.3	2550	9 US-10-123-910-59	Sequence 59, Appl
40	16.4	86.3	2550	9 US-10-124-813-59	Sequence 59, Appl
41	16.4	86.3	2550	9 US-10-124-817-59	Sequence 59, Appl
42	16.4	86.3	2550	9 US-10-124-824-59	Sequence 59, Appl
43	16.4	86.3	2550	9 US-10-125-922-59	Sequence 59, Appl
44	16.4	86.3	2550	9 US-10-125-924-59	Sequence 59, Appl
45	16.4	86.3	2550	9 US-10-127-825A-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-728-952-95
; Sequence 95, Application us/09728952
; Patent No. US2002011302A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunru
; APPLICANT: Yamazaki, Yuki
; APPLICANT: Ujwal, Manusha L.
; APPLICANT: Dimaac, Radoje T.
; TITLE OF INVENTION: No. US2002011302A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 799
; CURRENT APPLICATION NUMBER: US/09/728, 952
; CURRENT FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: pc_genes Version 2.0
; SEQ ID NO 95
; LENGTH: 1769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(1769)
US-09-728-952-95

Query Match 86.3%; Score 16.4; DB 10; Length 1769;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATCTGCTCTG 19
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Db 424 GCTCTGATCTGCTCTG 441

RESULT 2
US-10-028-072-59

Sequence 59, Application US/10028072
Publication No. US2003004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
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PRIOR APPLICATION NUMBER: 60/059117
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PRIOR FILING DATE: 1998-01-23
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PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
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PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07

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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088741
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; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTCTGATTCCTGCTCTG 19
Db      438 GCTCTGATTACTGCTCTG 455

RESULT 3
US-10-121-049-59
; Sequence 59, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/10/121,049
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-123-904-59

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTCTGATTCCTGCTCTG 19
Db      438 GCTCTGATTACTGCTCTG 455

RESULT 4
US-10-123-904-59
; Sequence 59, Application US/10123904
; Publication No. US2003002238A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-123-904-59

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

OY 2 GCTCGATTCTGCTCTG 19
|||||
Db 438 GCTCGATTACTGCTCTG 455

RESULT 5

US-10-140-470-59
; Sequence 59, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GCTCGATTCTGCTCTG 19
|||||
Db 438 GCTCGATTACTGCTCTG 455

RESULT 6

US-10-175-746-59
; Sequence 59, Application US/10175746
; Publication No. US2003002270A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-746-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GCTCGATTCTGCTCTG 19
|||||
Db 438 GCTCGATTACTGCTCTG 455

RESULT 7

US-10-176-918-59
; Sequence 59, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GCTCGATTCTGCTCTG 19
|||||
Db 438 GCTCGATTACTGCTCTG 455

RESULT 8

US-10-176-921-59
; Sequence 59, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C288
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
LENGTH: 2550
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-921-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCG 19
Db 438 GCTCTGATTCCTGCTCG 455

RESULT 9
US-10-137-865-59
Sequence 59, Application US/10137865
Publication No. US20030032155A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C154
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
LENGTH: 2550
TYPE: DNA
ORGANISM: Homo Sapien
US-10-137-865-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCTCTGATTCCTGCTCG 19
Db 438 GCTCTGATTCCTGCTCG 455

RESULT 10
US-10-140-474-59
Sequence 59, Application US/10140474
Publication No. US20030032156A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C162
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
LENGTH: 2550
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-474-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCG 19
Db 438 GCTCTGATTCCTGCTCG 455

RESULT 11
US-10-142-431-59
Sequence 59, Application US/10142431
Publication No. US20030036179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-431-59

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTCGATTCTGCTGCTG 19
         |||||
Db      438 GCTCGATTACTGCTGCTG 455

RESULT 12
US-10-143-114-59
; Sequence 59, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Zhanq, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-143-114-59

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTCGATTCTGCTGCTG 19
         |||||
Db      438 GCTCGATTACTGCTGCTG 455

RESULT 13
US-10-140-002-59
; Sequence 59, Application US/10140002
; Publication No. US20030037623A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

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; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Zhanq, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C244
; CURRENT APPLICATION NUMBER: US/10/142,419
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-419-59

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTCGATTCTGCTGCTG 19
         |||||
Db      438 GCTCGATTACTGCTGCTG 455

RESULT 14
US-10-142-419-59
; Sequence 59, Application US/10142419
; Publication No. US20030044945A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Zhanq, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C244
; CURRENT APPLICATION NUMBER: US/10/142,419
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-419-59

Query Match      86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCTGCTCTG 19
|||||
Db 438 GCTCTGATTACTGCTCTG 455

RESULT 15

US-10-123-262-59
; Sequence 59, Application US/10123262
; Publication No. US20030049816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Inc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C38
; CURRENT APPLICATION NUMBER: US/10/123,262
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-262-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;
Best Local Similarity 94.4%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCTGCTCTG 19
|||||
Db 438 GCTCTGATTACTGCTCTG 455

Search completed: June 21, 2003, 21:12:24
Job time : 122 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: June 21, 2003, 19:32:08 ; Search time 63 Seconds
(without alignments)
92.490 Million cell updates/sec

Title: US-09-581-500B-14

Perfect score: 19

Sequence: 1 cgctcgtatcctcgtctg 19

Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 441362 segs, 153338381 residues 882724

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/prodata/2/ina/5B COMB.seq:*

3: /cgn2_6/prodata/2/ina/6A COMB.seq:*

4: /cgn2_6/prodata/2/ina/6B COMB.seq:*

5: /cgn2_6/prodata/2/ina/PCtus COMB.seq:*

6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	83.2	1200	1	US-08-096-623A-19
C 2	15.8	83.2	71989	4	US-09-443-501A-2
C 3	15.8	83.2	246240	2	US-08-724-394A-20
C 4	15.8	83.2	246240	2	US-08-724-394A-21
C 5	15.8	83.2	246240	2	US-08-724-394A-22
C 6	15.4	81.1	1093	1	US-08-592-126-95
C 7	15.4	81.1	36519	3	US-08-923-137-2
C 8	15	78.9	1800	1	US-08-139-937-11
C 9	15	78.9	1800	5	PCT-US93-11310-11
C 10	14.8	77.9	2015	1	US-08-129-129-7
C 11	14.8	77.9	5232	4	US-08-972-927-1
C 12	14.8	77.9	7326	1	US-08-194-468-1
C 13	14.8	77.9	7326	4	US-09-514-247A-7
C 14	14.8	77.9	7344	4	US-08-961-739-1
C 15	14.8	77.9	7431	4	US-09-306-998-2
C 16	14.8	77.9	8147	4	US-09-514-247A-9
C 17	14.8	77.9	16063	4	US-09-801-052-3
C 18	14.8	77.9	45716	4	US-08-965-048-5
C 19	14.8	77.9	45988	4	US-08-965-048-6
C 20	14.4	75.8	1272	3	US-09-058-389A-7
C 21	14.4	75.8	1272	4	US-09-611-781-7
C 22	14.4	75.8	1847	3	US-09-058-389A-9
C 23	14.4	75.8	1847	4	US-09-611-781-9
C 24	14.4	75.8	2522	3	US-09-058-389A-1
C 25	14.4	75.8	2522	4	US-09-611-781-1
C 26	14.4	75.8	3489	2	US-08-728-323A-1
C 27	14.4	75.8	3489	4	US-09-298-568-1

28	14.4	75.8	3970	1	US-07-925-695-3	Sequence 3, Appl1
C 29	14.4	75.8	6354	3	US-09-058-389A-5	Sequence 5, Appl1
C 30	14.4	75.8	6354	4	US-09-611-781-5	Sequence 19, Appl1
C 31	14.4	75.8	6803	3	US-08-665-259-19	Sequence 1, Appl1
C 32	14.4	75.8	6803	2	US-08-955-138-1	Sequence 2, Appl1
C 33	14.4	75.8	9412	2	US-07-925-695-1	Sequence 2, Appl1
C 34	14.4	75.8	9589	1	US-07-925-695-2	Sequence 20, Appl1
C 35	14.4	75.8	9589	4	US-08-770-379-20	Sequence 11, Appl1
C 36	14.4	75.8	32207	2	US-08-757-669A-20	Sequence 11, Appl1
C 37	14.4	75.8	32207	4	US-09-230-371A-20	Sequence 11, Appl1
C 38	14.4	75.8	32207	3	US-08-808-881-11	Sequence 11, Appl1
C 39	14.2	74.7	36	3	US-09-017-631-11	Sequence 11, Appl1
C 40	14.2	74.7	36	3	US-08-383-743A-11	Sequence 11, Appl1
C 41	14.2	74.7	66	1	PCT-US93-07116-11	Sequence 3, Appl1
C 42	14.2	74.7	66	5	US-09-253-155A-55	Sequence 5, Appl1
C 43	14.2	74.7	529	1	US-08-390-858B-8	Sequence 8, Appl1
C 44	14.2	74.7	654	1		
C 45	14.2	74.7	654	1		

ALIGNMENTS

RESULT 1
US-08-096-623A-19/c
Sequence 19, Application US/08096623A
Patent No. 5684238
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
SURETY: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: AMO-006.1
TELECOMMUNICATION INFORMATION:

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

Query Match 83.2%; Score 15.8; DB 2; Length 246240;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCTCTGATTCCTGCTCTG 19
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Db 161737 CGCTCTGATTCGTCCTG 161755

RESULT 5
US-08-724-394A-22
Sequence 22, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Teuchhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.

REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match 83.2%; Score 15.8; DB 2; Length 246240;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCTCTGATTCCTGCTCTG 19
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Db 161737 CGCTCTGATTCGTCCTG 161755

RESULT 6
US-08-592-126-95/c
Sequence 95, Application US/08592126
Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 1093 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G164con.seq
US-08-592-126-95

Query Match 81.1%; Score 15.4; DB 1; Length 1093;

Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 GCTCGATTCCTGCTCT 18
Db 988 GCTCGATTCCTGCTCT 972

RESULT 7
US-08-923-137-2/c
Sequence 2, Application US/08923137
Patent No. 6083716
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Farina, Steven F.
APPLICANT: Fisher, Krishna J.
TITLE OF INVENTION: Chimpanzee Adenovirus Vectors
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,137
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,700
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVN.021CIPUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 36519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-923-137-2
Query Match 81.1%; Score 15.4; DB 3; Length 36519;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 CTCTGATTCCTGCTCTG 19
Db 23653 CTCTGATTCCTGCTCTG 23637
RESULT 8
US-08-139-937-11/c
Sequence 11, Application US/08139937
Patent No. 5821070
GENERAL INFORMATION:
APPLICANT: LEE, WEN-HWA
APPLICANT: SHAN, BEI
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 9370
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-139-937-11

Query Match 78.5%; Score 15; DB 1; Length 1800;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GCTCGATTCCTGCTCT 16
Db 1698 GCTCGATTCCTGCTCT 1684

RESULT 9
PCT-US93-11310-11/c
Sequence 11, Application PC/TUS9311310
GENERAL INFORMATION:
APPLICANT: BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11310
FILING DATE: 19-NOV-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-P-CJ 9790
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001

TELEX: 619-535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-11310-11

Query Match 78.9%; Score 15; DB 5; Length 1800;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTCTCT 16
DB 1698 GCTCTGATTCCTCTCT 1684

RESULT 10
US-08-129-129-7
Sequence 7, Application US/08129129
Patent No. 5767363
GENERAL INFORMATION:
APPLICANT: DE SILVA, Jacqueline
APPLICANT: SAFFORD, Richard
APPLICANT: HUGHES, Stephen Glynn
TITLE OF INVENTION: PLANT PROMOTER INVOLVED IN
TITLE OF INVENTION: CONTROLLING LIPID BIOSYNTHESIS IN SEEDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,129
FILING DATE: 18-JAN-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91303098.7
FILING DATE: 09-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00627
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 203424/T7016(C)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 994..1938
US-08-129-129-7

Query Match 77.9%; Score 14.8; DB 1; Length 2015;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCTG 19
DB 1468 GCTCTGATTCCTGCTCTG 1485

RESULT 11
US-08-972-927-1
Sequence 1, Application US/08972927
Patent No. 6166290
GENERAL INFORMATION:
APPLICANT: Rea, Philip A
APPLICANT: Lu, Yu-Ping
APPLICANT: Li, Ze-Sheng
TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZ JACOBS & NADIEL, P.C.
STREET: One Commerce Square, 2005 Market Street, 22nd
STREET: Floort
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: US
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,927
FILING DATE: 18-NOV-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,040
FILING DATE: 18-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/061,328
FILING DATE: 08-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Doyle Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596-1202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5232 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-972-927-1

Query Match 77.9%; Score 14.8; DB 4; Length 5232;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCTG 19
DB 1259 GCTCTGATTCCTGCTCTG 1276

RESULT 12
US-08-194-468-1/C
Sequence 1, Application US/08194468

```

; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Preity, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7326 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7323
; US-08-194-468-1

Query Match          77.9%; Score 14.8; DB 1; Length 7326;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCTGTGATTCCTGCTCTG 19
Db      3136 GCTGTGACTTCTGCTCTG 3119

RESULT 13
US-09-514-247A-7/c
; Sequence 7, Application US/09514247A
; Patent No. 6365361
; GENERAL INFORMATION:
; APPLICANT: TANABE SEIYAKU CO. LTD.
; APPLICANT: TANIGUCHI, Tomoyasu
; APPLICANT: MIZUKAMI, Junko
; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
; FILE REFERENCE: TANIGUCHI=6
; CURRENT APPLICATION NUMBER: US/09/514,247A
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT/JP98/03734
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: JP231084/1997
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 7326

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; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7326)
; OTHER INFORMATION: n at position 1131 is unknown.
; US-09-514-247A-7

Query Match          77.9%; Score 14.8; DB 4; Length 7326;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCTGTGATTCCTGCTCTG 19
Db      3136 GCTGTGACTTCTGCTCTG 3119

RESULT 14
US-08-961-739-1/c
; Sequence 1, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7326
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7326)
; NAME/KEY: misc feature
; LOCATION: (1)..(7326)
; OTHER INFORMATION: n = A,T,C or G
; US-08-961-739-1

Query Match          77.9%; Score 14.8; DB 3; Length 7344;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCTGTGATTCCTGCTCTG 19
Db      3136 GCTGTGACTTCTGCTCTG 3119

RESULT 15
US-09-306-998-2
; Sequence 2, Application US/09306998
; Patent No. 6291173
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: MMS2
; FILE REFERENCE: MMS2- An MMS1 Interacting Protein
; CURRENT APPLICATION NUMBER: US/09/306,998
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 60/084,740
; EARLIER FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 7431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 18:29:33 ; Search time 215 Seconds
(without alignments)
199.014 Million cell updates/sec

Title: US-09-581-500B-14

Perfect score: 19

Sequence: 1 cgcctcgtatccctcctcgt 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 segs, 112599155 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	100.0	19	20	AAx88558	Human chromosome 1
2	19	100.0	656	20	AAx88553	Human chromosome 1
3	17	89.5	112460	24	ABK83567	Human cDNA differe
4	16.4	86.3	502	22	AAFP3539	Lung carcinoma CDN
5	16.4	86.3	511	22	AAFP3542	Lung carcinoma CDN
6	16.4	86.3	857	22	AAH08486	Human cDNA clone (
7	16.4	86.3	1769	24	ABK94976	Human novel polyu
8	16.4	86.3	1873	22	AAH13543	Human cDNA sequenc
9	16.4	86.3	2252	22	AAH16597	Human cDNA sequenc

10	16.4	86.3	2550	22	AA521272	Human cDNA sequenc
11	16.4	86.3	2609	21	AAH80606	Human secreted pro
12	16.4	86.3	3185	22	AAAD05402	Human secreted pro
13	16.4	86.3	125439	24	ABO08177	Human osteoblast d
14	15.8	83.2	60	24	ABM45912	Human spliced tran
15	15.8	83.2	151	16	AACT24088	Human gene signatu
16	15.8	83.2	227	24	ABNT75155	Human ORF102 cDNA,
17	15.8	83.2	1200	12	AAQ13726	Zeaxanthin glycosy
18	15.8	83.2	1391	24	ABN97245	Gene #3743 used to
19	15.8	83.2	1391	24	ABK64813	Human benign prost
20	15.8	83.2	1391	24	ABL69614	Prostate cancer re
21	15.8	83.2	2977	22	AAK94355	Human full-length
22	15.8	83.2	7180	22	AAK75761	Human immune/haema
23	15.8	83.2	10126	22	AAK35829	Human musculoskele
24	15.8	83.2	71989	21	AAA29349	Sorangium cellulos
25	15.8	83.2	235033	19	AAV57926	Hereditary haemoch
26	15.8	83.2	237326	19	AAV59093	Hereditary haemoch
27	15.8	83.2	302250	24	ABL67703	Oesophagus cancer
28	15.8	83.2	319608	21	AAH51601	Human chromosome 1
29	15.8	83.2	319608	22	AA509301	Human schizopreni
30	15.4	81.1	322	22	AAK36191	Human musculoskele
31	15.4	81.1	700	22	AAH92619	Human inflammatory
32	15.4	81.1	975	24	AAH74153	Bovine embryonic g
33	15.4	81.1	1093	19	AAV60020	Nucleic acid G164C
34	15.4	81.1	1267	22	AAH21012	Bovine-derived DNA
35	15.4	81.1	1333	21	AAK46183	Arabidopsis thalia
36	15.4	81.1	1336	21	AAK34766	Arabidopsis thalia
37	15.4	81.1	1405	20	AAV84549	Human secreted pro
38	15.4	81.1	1405	22	ABA83332	Human secreted pro
39	15.4	81.1	3821	20	AAK34365	Human nerve growth
40	15.4	81.1	3821	24	AAH030143	Human nerve growth
41	15.4	81.1	3821	24	ABA92502	Human nerve growth
42	15.4	81.1	3995	24	ABK35489	Human endometrial
43	15.4	81.1	3995	24	ABK35548	Gene D1G4 differen
44	15.4	81.1	4066	23	ABL11003	Drosophila melanog
45	15.4	81.1	6087	22	AA522683	Human cDNA encodin

ALIGNMENTS

RESULT 1	AAx88558	Human chromosome 18q YAC clone amplification primer.
ID	AAx88558	standard; DNA; 19 BP.
AC	AAx88558;	
XX		
DT	10-SEP-1999	(first entry)
DE		Human chromosome 18q YAC clone amplification primer.
XX		
XX		Human chromosome 18q; mood disorder; polymorphic marker; detection;
XX		identification; trinucleotide repeat expansion; schizophrenia;
KM		anxiety disorder; adjustment disorder; personality disorder;
KM		nucleotide triplet repeat; ss.
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
XX	W09932643-A2.	
XX		
PD	01-JUL-1999.	
XX		
XX	17-DEC-1998;	98WO-EP08543.
XX		
ER	18-DEC-1997;	97GB-0026804.
XX		
PA	(VIAA-) VIAAMS INTERUNIVERSITAIR INST BIOTECNOC.	
XX		
PI	Del-Favero J, Raeymaekers P, Van Broeckhoven C;	
XX		
DR	WPI; 1999-418934/35.	
XX		

PT Detecting nucleotide triplet repeats in human chromosome 18q
 XX Claim 29, Fig 15b, 87pp; English.
 CC The present invention describes detecting nucleotide triplet repeats in
 CC a region of human chromosome 18q disposed between polymorphic markers
 CC D18S68 and D18S979 to identify a human gene associated with a mood
 CC disorder or related disorder. AAX88542 to AAX88705 represents human
 CC chromosome 18q YAC clones and primers corresponding to them, used in the
 CC exemplification of the present invention. YAC clones comprising a
 CC portion of the region of human chromosome 18q between markers D18S68 and
 CC D18S979 are used to identify at least one human gene associated with a
 CC mood disorder or related disorder. The mood disorder or related
 CC disorder, is chosen from the Diagnostic and Statistical Manual of Mental
 CC Disorders, Version 4 (DSM-IV) taxonomy. This includes mood disorders
 CC (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related
 CC disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX,
 CC 309.81, 308.3), adjustment disorders (309.XX) and personality disorders
 CC (codes 301.XX). Probes derived from genes associated with the mood
 CC disorder or related disorder can be used to detect pathological
 CC mutations or genetic variations in patients. The methods, probes and
 CC antibodies can be used to determine the susceptibility of an individual
 CC to a mood disorder or related disorder. The nucleic acids and proteins
 CC of the human gene can be used to treat mood disorders and related
 CC disorders.

Sequence 19 BP, 1 A; 7 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 1 CGCTCGATTCGCTCTG 19
 |||||
 Db 1 CGCTCGATTCGCTCTG 19

RESULT 2

AAX88553/c
 ID AAX88553 standard; DNA; 656 BP.

AC AAX88553;

DT 10-SEP-1999 (first entry)

DE Human chromosome 18q YAC clone nucleotide sequence #12.

KW Human chromosome 18q; mood disorder; polymorphic marker; detection;

KW identification; trinucleotide repeat expansion; schizophrenia;

KW anxiety disorder; adjustment disorder; personality disorder;

KW nucleotide triplet repeat; ss.

OS Homo sapiens.

OS Synthetic.

PN WO9932643-A2.

PD 01-JUL-1999.

PF 17-DEC-1998; 98WO-EP08543.

PR 18-DEC-1997; 97GB-0026804.

PA (VIAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Del-Favero J, Raeymaekers P, Van Broeckhoven C;

DR WPI; 1999-418934/35.

PT Detecting nucleotide triplet repeats in human chromosome 18q

PS Claim 21, Fig 15a, 87pp; English.

CC The present invention describes detecting nucleotide triplet repeats in
 CC a region of human chromosome 18q disposed between polymorphic markers
 CC D18S68 and D18S979 to identify a human gene associated with a mood
 CC disorder or related disorder. AAX88542 to AAX88705 represents human
 CC chromosome 18q YAC clones and primers corresponding to them, used in the
 CC exemplification of the present invention. YAC clones comprising a
 CC portion of the region of human chromosome 18q between markers D18S68 and
 CC D18S979 are used to identify at least one human gene associated with a
 CC mood disorder or related disorder. The mood disorder or related
 CC disorder, is chosen from the Diagnostic and Statistical Manual of Mental
 CC Disorders, Version 4 (DSM-IV) taxonomy. This includes mood disorders
 CC (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related
 CC disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX,
 CC 309.81, 308.3), adjustment disorders (309.XX) and personality disorders
 CC (codes 301.XX). Probes derived from genes associated with the mood
 CC disorder or related disorder can be used to detect pathological
 CC mutations or genetic variations in patients. The methods, probes and
 CC antibodies can be used to determine the susceptibility of an individual
 CC to a mood disorder or related disorder. The nucleic acids and proteins
 CC of the human gene can be used to treat mood disorders and related
 CC disorders.

Sequence 656 BP, 183 A; 165 C; 208 G; 96 T; 4 other;

Query Match 100.0%; Score 19; DB 20; Length 656;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 1 CGCTCGATTCGCTCTG 19
 |||||
 Db 533 CGCTCGATTCGCTCTG 515

RESULT 3

ABX83567
 ID ABX83567 standard; cDNA; 112460 BP.

AC ABX83567;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #138.

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;

KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; streptococcal infection; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;

KW granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

PN WO200228999-A2.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US30821.

PR 03-OCT-2000; 2000US-237189P.

PA (GENE-) GENA LOGIC INC.

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

DR WPI; 2002-435328/46.

PT Detecting granulocyte activation by detecting differential expression

PS of genes associated with granulocyte activation, which serves as

PT diagnostic markers that is useful for monitoring disease states and

PT drug toxicity

PS Claim 1; SEQ ID No 138; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC or allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease, also bacterial infection, viral infection, and MS is
 CC parasitic infection, protozoal infection, fungal infection and MS is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 XX Sequence 112460 BP; 24087 A; 29523 C; 31203 G; 27647 T; 0 other;

XX
 XX Query Match 89.5%; Score 17; DB 24; Length 112460;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 XX 3 CTCGATTCCTGCTCTG 19
 XX |||||
 XX 88792 CTCGATTCCTGCTCTG 88808

XX
 XX RESULT 4
 XX AAF93539
 XX ID AAF93539 standard; cDNA; 502 BP.

XX
 XX AC AAF93539;
 XX AT 21-MAY-2001 (first entry)

XX
 XX DE Lung carcinoma cDNA encoding SRT protein SEQ ID 360.

XX
 XX KM Human; SRT; gene therapy; gene mapping; tissue typing; ss.

XX
 XX OS Homo sapiens.

XX
 XX PN WO200107611-A2.

XX
 XX PD 01-FEB-2001.

XX
 XX PF 21-JUL-2000; 2000WO-US20006.

XX
 XX PR 26-JUL-1999; 99US-0145701.

XX
 XX PA (SETH) GENENTECH INC.

XX
 XX Baker KP, Goddard A, Wood WI;
 XX WPI; 2001-112729/12.

XX
 XX PT New isolated nucleic acid molecule encoding a SRT polypeptide is useful
 XX for production of recombinant SRT polypeptides, gene mapping,
 XX PT diagnosing genetic disorders and for gene therapy -

XX
 XX PS Claim 2; Fig 360; 663pp; English.

XX
 XX Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
 XX human SRT proteins. The cDNA sequences are isolated from various
 XX different human tissue cDNA libraries. The invention relates to a method
 XX for detecting cDNA encoding an SRT protein, a vector containing cDNA
 XX encoding SRT, a host cell transformed with the vector, an isolated SRT
 XX polypeptide, and an antibody which binds to SRT. The polynucleotide
 XX sequence can be used in gene therapy and is useful in the recombinant
 XX production of SRT polypeptides, as a hybridisation probe to screen
 XX libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
 XX map the gene encoding the SRT polypeptides and analysing genetic
 XX disorders, tissue typing and disease tissue detection. The SRT
 XX polynucleotide sequences can be used in polymerase chain reaction,
 XX screening for new therapeutic molecules and generation of antisense RNA
 XX and DNA.

XX
 XX Sequence 502 BP; 94 A; 149 C; 119 G; 131 T; 9 other;

XX
 XX Query Match 86.3%; Score 16.4; DB 22; Length 502;
 XX Best Local Similarity 94.4%; Pred. No. 3.2e+02;
 XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 XX 2 GCTCGATTCCTGCTCTG 19
 XX |||||
 XX 400 GCTCGATTCCTGCTCTG 417

XX
 XX RESULT 5
 XX AAF93542
 XX ID AAF93542 standard; cDNA; 511 BP.

XX
 XX AC AAF93542;
 XX AT 21-MAY-2001 (first entry)

XX
 XX DE Lung carcinoma cDNA encoding SRT protein SEQ ID 363.

XX
 XX KM Human; SRT; gene therapy; gene mapping; tissue typing; ss.

XX
 XX OS Homo sapiens.

XX
 XX PN WO200107611-A2.

XX
 XX PD 01-FEB-2001.

XX
 XX PF 21-JUL-2000; 2000WO-US20006.

XX
 XX PR 26-JUL-1999; 99US-0145701.

XX
 XX PA (SETH) GENENTECH INC.

XX
 XX Baker KP, Goddard A, Wood WI;
 XX WPI; 2001-112729/12.

XX
 XX PT New isolated nucleic acid molecule encoding a SRT polypeptide is useful
 XX for production of recombinant SRT polypeptides, gene mapping,
 XX PT diagnosing genetic disorders and for gene therapy -

XX
 XX PS Claim 2; Fig 363; 663pp; English.

XX
 XX Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
 XX human SRT proteins. The cDNA sequences are isolated from various

SQ Sequence 511 BP; 98 A; 168 C; 119 G; 126 T; 0 other;

QY 2 GCTCTGATTCCTGCTCTG 19
|||||
Db 445 GCTCTGATTACTGCTCTG 462

RESULT 6
AAH08486
ID AAH08486 standard; cDNA; 857 BP.

DT	26-JUN-2001 (first entry)	
XX		
DE	Human cDNA clone (5'-primer)	SEQ ID NO:5321

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

PN EP1074617-A2

PD 07-FEB-2001.

PF 28-JUL-2000;

PR 29-JUL-1999

PR 11-JAN-2000;

PR. 09-JUN-2000;

PA (HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J, PI

[illegible]

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PT full-length cDNAs defined in the specification, and for the detection

PT	full-length cDNAs -
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100	100

PS Claim 1; SEQ ID 5321; 2537pp + CD ROM; English

CC The present invention describes primer sets for synthesising 5602
CC
CC

comprises: (a) an oligo-dT primer and an oligonucleotide compleme

CC the 5602 nucleotide sequences defined in the specification, where the

CC of an oligonucleotide comprising a sequence complementary to the

'CC sequence and an oligonucleotide comprising a sequence complementary to a

Sequence 857 BP; 196 A; 235 C; 221 G; 201 T; 4 other;

2y 2 GCTCTGATTCTGCTCTG 19
 |||||
 Db 141 GCTCTGATTCTGCTCTG 158

RESULT 7
ABK94976
ID ABK94976 standard; cDNA; 1769 BP.

DT	30-AUG-2002 (first entry)
XX	
DE	Human novel polynucleotide #87

KW Human; gene; ss; inflammatory condition; shock; sepsis; immune response;

KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon

KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;

KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;

KW fungal infection.

OS Homo sapiens

PN WO200244340-A2

PD 06-JUN-2002.

30-NOV-2001; 2001W0-US47004.

PR 30-NOV-2000; 2000US-0028952.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;

XX

DR P-PSDB; ABG66752.

PT Novel nucleic acids and polypeptides for diagnosis, treatment of

PT disorders, cancer and promoting wound healing -

PS Claim 1; Page 546-548; 672pp; English

CC The invention relates to human novel polynucleotides and associated

CC treating inflammatory conditions such as arthritis, nephritis, Crohn's

CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of hematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
CC and coagulation disorders. Sequences ABK94890-ABK94982 represent human
CC novel polynucleotides of the invention.

SQ Sequence 1769 BP; 389 A; 480 C; 483 G; 417 T; 0 other;

Query Match 86.3%; Score 16.4; DB 24; Length 1769;

Best Local Similarity 94.4%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 GGTCTGATTCCTGCTCTG 19
424 GGTCTGATTCCTGCTCTG 441

RESULT 8

AAH13643/c
ID AAH13643 standard; cDNA; 1873 BP.

AAH13643;

26-JUN-2001 (first entry)

Human cDNA sequence SEQ ID NO:10485.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens.

EP1074617-A2.

07-FEB-2001.

28-JUL-2000; 2000EP-0116126.

29-JUL-1999; 99JP-0248036.

27-AUG-1999; 99JP-0300253.

11-JAN-2000; 2000JP-0118776.

02-MAY-2000; 2000JP-0183767.

09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J,

Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602

full-length cDNAs defined in the specification, and for the detection

and/or diagnosis of the abnormality of the proteins encoded by the

full-length cDNAs -

Claim 8; SEQ ID 10485; 2537pp + CD ROM; English.

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH1628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 1873 BP; 549 A; 419 C; 526 G; 379 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 1873;

Best Local Similarity 94.4%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 GGTCTGATTCCTGCTCTG 19
914 GGTCTGATTCCTGCTCTG 897

RESULT 9

AAH16697
ID AAH16697 standard; cDNA; 2252 BP.

AAH16697;

26-JUN-2001 (first entry)

Human cDNA sequence SEQ ID NO:15859.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens.

EP1074617-A2.

07-FEB-2001.

28-JUL-2000; 2000EP-0116126.

29-JUL-1999; 99JP-0248036.

27-AUG-1999; 99JP-0300253.

11-JAN-2000; 2000JP-0118776.

02-MAY-2000; 2000JP-0183767.

09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J,

Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602

full-length cDNAs defined in the specification, and for the detection

and/or diagnosis of the abnormality of the proteins encoded by the

full-length cDNAs -

Claim 8; SEQ ID 15859; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602

22-FEB-2000; 2000WO-US04414
24-FEB-2000; 2000WO-US04914

KM Secreter protein, immunosuppressant; anti-inflammatory; antiarthritic;
KM antirheumatic; dermatological; antiproliferative; antiatherosclerotic;
KM anticancer; vulnerary; antiviral; antibacterial; antifungal;
KM immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;

KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human; ss.
 OS Homo sapiens.
 PN WO200029435-A1.
 XX
 XX 25-MAY-2000.
 PD
 XX 27-OCT-1999; 99WO-US25031.
 PF
 XX 28-OCT-1998; 98US-0105971.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Ni J, Ruben SM, Olsen HS, Young PE, Kenny JT, Moore PA, Wei Y;
 PI Greene JM;
 XX
 XX MPI; 2000-387742/33.
 DR P-PSDB; AAB25576.
 XX
 PT Isolated nucleic acid molecules encoding human secreted proteins are
 PT used for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases -
 XX
 PS Claim 1; Figure 1A-C; 803pp; English.
 XX
 CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given
 CC in AAB0606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant;
 CC anti-inflammatory; antirheumatic; antineoplastic; dermatological;
 CC antiproliferative; antiarteriosclerotic; anticancer; antiviral;
 CC antiviral; antibacterial; and antifungal activity. The proteins,
 CC polypeptides, agonists and antagonists may be used to treat prevent
 CC and/or diagnose various disease, disorders and conditions examples of
 CC which include: immune disorders e.g. Addison's disease, rheumatoid
 CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
 CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;
 CC hyperproliferative disorders such as parapsoriasis and psoriasis;
 CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
 CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
 CC sequences may also be used in wound healing and the treatment of
 CC infectious diseases. The human secreted protein gene #1 and protein
 CC sequences are represented in sequences AAB0606 and AAB25576. Also given
 CC is an alternative protein product of human secreted protein gene #1 in
 CC AAB25594.
 XX
 SQ Sequence 2609 BP; 682 A; 658 C; 680 G; 589 T; 0 other;
 Query Match 86.3%; Score 16.4; DB 21; Length 2609;
 Best Local Similarity 94.4%; Pred. No. 3.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GCTCGATTCTGCTCTG 19
 DB 411 GCTCGATTCTGCTCTG 428
 XX
 RESULT 12
 AAD054402/c
 ID AAD054402 standard; cDNA; 3185 BP.
 AC AAD054402;
 XX
 XX 17-JUL-2001 (first entry)
 DT
 XX Human secreted protein-encoding gene 14 cDNA clone HPUBK11, SEQ ID NO:24.
 DE

XX Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vunerary;
 KW cell culture; chemotaxis; food additive; chromosome 9;
 KW binding partner identification; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 169..459
 FT /*tag= a
 FT /product= "human secreted protein"
 FT sig_peptide 169..252
 FT /*tag= b
 FT mat_peptide 253..456
 FT /*tag= c
 FT /product= "mature human secreted protein"
 FT
 XX WO200134623-A1.
 PN
 XX 17-MAY-2001.
 PD
 XX 01-NOV-2000; 2000WO-US30037.
 PF
 XX 05-NOV-1999; 99US-0163577.
 PR 30-JUN-2000; 2000US-0215137.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Komatsuolis GA, Moore PA;
 PI
 XX MPI; 2001-316490/33.
 DR P-PSDB; AAB01559.
 DR
 XX Nucleic acids encoding 29 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 PT
 XX
 PS Claim 1; Page 423-424; 535pp; English.
 XX
 CC AAD0389-AAD05473 represent cDNAs corresponding to 29 human secreted
 CC protein genes, and AAB01546-AAB01630 represent the proteins they encode.
 CC AAB01631-AAB01660 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 29 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and

CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein-encoding cDNA of the invention.

XX Sequence 3185 BP, 772 A, 808 C, 890 G, 715 T, 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 3185;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCTG 19

Db 1515 GCTCAGATTCCTGCTCTG 1498

RESULT 13
ABQ88177/C
ID ABQ88177 standard; cDNA; 125439 BP.

XX ABQ88177;

DT 18-SEP-2002 (first entry)

DE Human osteoblast differentiation related cDNA SEQ ID NO 84.

XX Human; osteoblast; stem cell differentiation; bone tissue deposition;

KW osteoporosis; osteopachic; ss.

XX Homo sapiens.

XX WO200250301-A2.

PD 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US48276.

XX 18-DEC-2000; 2000US-255882P.

PR 24-APR-2001; 2001US-285691P.

XX (GENE-) GENE LOGIC INC.

PA (PROCT) PROCTER & GAMBLE CO.

PI J1 D, Axelrod DW, Cook JS, Talswal N, Einstein R, Houghton A;

XX WPI; 2002-557663/59.

PT Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosing
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process

XX Claim 1; SEQ ID NO 84; 78bp + Sequence listing; English.

XX The invention relates to genes and their expression profiles are used
XX for:

CC (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;

CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC osteoblast formation or osteoporosis; or

CC (c) treating or monitoring treatment of the conditions cited in (b), or
CC monitoring the progression of bone tissue deposition.

CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,

CC drug-induced abnormalities in bone formation or bone loss, conditions
CC that involve altered bone metabolism (e.g. idiopathic juvenile

CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC Panconi syndrome or fibrous dysplasia. The present sequence is that of an

CC osteoblast differentiation associated cDNA marker of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 125439 BP; 32323 A; 32592 C; 30004 G; 30520 T; 0 other;

Query Match 86.3%; Score 16.4; DB 24; Length 125439;
Best Local Similarity 94.4%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCTG 19

Db 49494 GCTCTGATTCCTGCTCTG 49477

RESULT 14
ABN45912/C
ID ABN45912 standard; DNA; 60 BP.

XX ABN45912;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:18660.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

PD 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes

XX Example 1; SEQ ID 18660; 47bp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple

XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a

XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.

XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or

XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal

XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a

XX particular biological or pathological state, and so allowing the
XX detection of tissue- or pathology-specific genes such as those genes

XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA

XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent

XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.

XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 60 BP; 9 A; 17 C; 18 G; 16 T; 0 other;

Query Match 83.2%; Score 15.8; DB 24; Length 60;
Best Local Similarity 89.5%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCTGATTCCTGCTG 19
|||||
DB 50 CGCTGATTCCTGCTG 32

RESULT 15

AAT24088/c
ID AAT24088 standard; cDNA to mRNA; 151 BP.

AC AAT24088;

DT 06-SEP-1996 (first entry)

DE Human gene signature HMG806076.

XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;

KW human; cloning; mapping; non-biased library; diagnosis; detection;

XX cell typing; abnormal cell function; ss.

OS Homo sapiens.

XX MO9514772-A1.

XX 01-JUN-1995.

XX 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

PA (MATS/) MATSUBARA K.

PI (OKUB/) OKUBO K.

XX Matsubara K, Okubo K;

XX WPI; 1995-206931/27.

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.

PT for diagnosis of abnormal cell function, by preparing cDNA that

PT reflects relative abundance of corresp. mRNA in specific human

PT tissues

PS Claim 1; Page 1527; 2245bp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp.

XX double-stranded DNA) which comprises one of the 7837 "GS" sequences

XX given in AAT19001-T26837 and which is able to hybridise to part of

XX human genomic DNA. cDNA or mRNA is claimed. The GS (Gene Signature)

XX sequences were obtained from 3'-directed cDNA libraries prepared

XX from various human tissues; synthesis of cDNA was initiated from the

XX 3'-end of mRNA by using poly(U) as the sole primer. Since the 3'-

XX untranslated sequence is unique to a particular mRNA species, almost

XX all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

XX is constructed so as to reflect accurately the relative abundance of

XX different mRNAs in the particular tissue from which it was derived.

XX The appearance frequency of a given GS in a cDNA library can be

XX determined (esp. using primers and probes derived from the GS

XX sequences) as a means of diagnosing abnormal cell function or for

XX recognising different cell types.

XX SQ Sequence 151 BP; 49 A; 33 C; 39 G; 29 T; 1 other;

DB 25 CGCTGATTCCTGCTG 7

Search completed: June 21, 2003, 19:39:34
Job time : 218 secs

Query Match 83.2%; Score 15.8; DB 16; Length 151;

Best Local Similarity 89.5%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCTGATTCCTGCTG 19
|||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 18:31:18 ; Search time 991 Seconds
(without alignments)
557.975 Million cell updates/sec

Title: US-09-581-500B-14

Perfect score: 19

Sequence: 1 cgcctcgtatccctcgcctcg 19

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmb1.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_hg_hum.*
31: em_hg_inv.*
32: em_hg_other.*
33: em_hg_mus.*
34: em_hg_pla.*
35: em_hg_rod.*
36: em_hg_mam.*
37: em_hg_vrt.*
38: em_sy.*
39: em_hggo_hum.*
40: em_hggo_mus.*
41: em_hggo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	AX021008	AX021008 Sequence
2	19	100.0	656	AX021006	AX021006 Sequence
3	19	100.0	186351	AP001503	AP001503 Homo sapi
4	19	100.0	181385	AC009802	AC009802 Homo sapi
5	19	100.0	191793	AP001897	AP001897 Homo sapi
6	19	100.0	198291	AC067875	AC067875 Homo sapi
7	19	100.0	201734	AC090224	AC090224 Homo sapi
8	17.4	91.6	2121	AF140243	AF140243 Xenopus 1
9	17.4	91.6	151130	AC127432	AC127432 Mus muscu
10	17.4	91.6	111395	AC128860	AC128860 Rattus no
11	17.4	91.6	168369	AC119463	AC119463 Rattus no
12	17.4	91.6	176054	AC022377	AC022377 Homo sapi
13	17.4	91.6	178548	AC018831	AC018831 Homo sapi
14	17.4	91.6	189040	AC125748	AC125748 Rattus no
15	17.4	91.6	192180	AL845471	AL845471 Homo sapi
16	17.4	91.6	196044	AC018505	AC018505 Homo sapi
17	17.4	91.6	198587	AC026218	AC026218 Homo sapi
18	17.4	91.6	198808	AC129207	AC129207 Mus muscu
19	17.4	91.6	202844	AC090956	AC090956 Homo sapi
20	17.4	91.6	203026	AL772271	AL772271 Mus muscu
21	17.4	91.6	204412	AC021446	AC021446 Mus muscu
22	17.4	91.6	205925	AC009711	AC009711 Homo sapi
23	17.4	91.6	209876	AC011599	AC011599 Homo sapi
24	17.4	91.6	229402	AC069271	AC069271 Homo sapi
25	17.4	91.6	256657	AC129177	AC129177 Mus muscu
26	17.4	89.5	12693	U58729	U58729 Caenorhabdi
27	17	89.5	112460	HS1104E15	AL022312 Human DNA
28	17	89.5	159659	2	AC116868 Mus muscu
29	17	89.5	169193	2	AC068523 Homo sapi
30	17	89.5	176526	2	AP005230 Homo sapi
31	17	89.5	196500	2	AC068734 Homo sapi
32	17	89.5	208844	2	AC118200 Mus muscu
33	17	89.5	262387	10	AL670959 Mus muscu
34	16.4	86.3	305	11	AU027365 Rattus no
35	16.4	86.3	502	6	AX079616 Sequence
36	16.4	86.3	511	6	AX079619 Sequence
37	16.4	86.3	540	8	CNS01B18
38	16.4	86.3	901	11	CNS06EK4
39	16.4	86.3	1268	9	BC015201
40	16.4	86.3	1873	9	AK000870
41	16.4	86.3	2252	9	AK023902
42	16.4	86.3	2343	10	BC034347
43	16.4	86.3	2514	9	BC016552
44	16.4	86.3	2550	6	AX463926
45	16.4	86.3	2638	10	BC025476

ALIGNMENTS

RESULT 1
AX021008
LOCUS AX021008
DEFINITION Sequence 14 from Patent W0932643.
ACCESSION AX021008
VERSION AX021008.1 GI:10044671
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Del-Favero J., Raeymaekers P. and Van Broeckhoven, C.
TITLE Mood disorder gene
JOURNAL Patent: WO 9932643-A 14 01-JUL-1999;

BROECKHOVEN CHRISTINE VAN (BE); DEL PAVERO JURGEN (BE); RAEYMAEKERS
 PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
 FEATURES
 SOURCE 1.19 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 1 a 7 c 4 g 7 t
 ORIGIN
 Query Match 100.0%; Score 19; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 19; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 CGCTCGATTCCTGCTCG 19
 Db 1 CGCTCGATTCCTGCTCG 19
 RESULT 2
 AX021006/c 656 bp DNA linear PAT 07-SEP-2000
 LOCUS
 DEFINITION Sequence 12 from Patent WO9932643.
 ACCESSION AX021006
 VERSION AX021006.1 GI:10044669
 KEYWORDS
 SOURCE human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 656)
 del-Pavero,J., Raeymaekers,P. and Van Broeckhoven,C.
 TITLE
 Mood disorder gene
 JOURNAL
 Patent: WO 9932643-A 12 01-JUL-1999;
 BROECKHOVEN CHRISTINE VAN (BE); DEL PAVERO JURGEN (BE); RAEYMAEKERS
 PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
 FEATURES
 SOURCE 1.656
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 183 a 165 c 208 g 96 t 4 others
 ORIGIN
 Query Match 100.0%; Score 19; DB 6; Length 656;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCTCGATTCCTGCTCG 19
 Db 533 CGCTCGATTCCTGCTCG 515
 RESULT 3
 AP001503/c 186351 bp DNA linear HNG 30-MAY-2000
 LOCUS
 DEFINITION Homo sapiens chromosome 18 clone RP11-879N20 map 18q22, WORKING
 DRAFT SEQUENCE, 23 unordered pieces.
 ACCESSION AP001503
 VERSION AP001503.2 GI:8117361
 HTG: HTGS PHASE1, HTGS DRAFT.
 KEYWORDS
 SOURCE Homo sapiens DNA, clone:RP11-879N20.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 186351)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Torokiy,Y., Matanabe,H. and Sakaki,Y.
 TITLE
 Published Only in Database (2000)
 JOURNAL
 2 (bases 1 to 186351)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Torokiy,Y., Matanabe,H. and Sakaki,Y.
 AUTHORS
 Direct Submission
 JOURNAL
 Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical

COMMENT

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
 Japan (E-mail:hattori@gs.c.riken.go.jp)
 URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
 Fax:81-42-778-9924)
 On May 30, 2000 this sequence version replaced gi:728819.
 ----- Genome Center -----
 Center: RIKEN Genomic Sciences Center(GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gs.c.riken.go.jp
 ----- Project Information -----
 Center project name: HumDraf18
 Center clone name: RP11-879N20
 ----- Summary Statistics -----
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 162162 bases at least Q40
 Consensus quality: 175389 bases at least Q30
 Consensus quality: 181326 bases at least Q20
 Insert size: 184151, sum-of-contrigs
 Quality coverage: 4.54x in Q20 bases; sum-of-contrigs

 NOTE: This is a 'working draft' sequence. It currently consists of
 23 contrigs. The true order of the pieces is not known and their
 order in this sequence record is arbitrary. Gaps between the
 contrigs are represented as runs N, but the exact sizes of the gaps
 are unknown. This record will be updated with the finished sequence
 as soon as it is available and the accession number will be
 preserved.
 1 42519 contrig of 42519 bp in length
 42620 59852 contrig of 17233 bp in length
 59953 74496 contrig of 14544 bp in length
 74597 87440 contrig of 12844 bp in length
 87541 99577 contrig of 12037 bp in length
 99678 110659 contrig of 10982 bp in length
 110760 115413 contrig of 4654 bp in length
 115514 124990 contrig of 9477 bp in length
 125091 135744 contrig of 10654 bp in length
 135845 145972 contrig of 10128 bp in length
 146073 153170 contrig of 7098 bp in length
 153271 156398 contrig of 3128 bp in length
 156499 161724 contrig of 5226 bp in length
 161825 165688 contrig of 3844 bp in length
 165789 169698 contrig of 3910 bp in length
 169799 173554 contrig of 37354 bp in length
 173655 175764 contrig of 2110 bp in length
 175865 177303 contrig of 1439 bp in length
 177404 179097 contrig of 1694 bp in length
 179198 181636 contrig of 2439 bp in length
 181737 183644 contrig of 1908 bp in length
 183745 184761 contrig of 1017 bp in length
 184862 186351 contrig of 1440 bp in length
 Sequence updated (26-May-2000).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 23 contrigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contrigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 42519: contrig of 42519 bp in length
 * 42520 42619: gap of 100 bp
 * 42620 59852: contrig of 17233 bp in length
 * 59853 59952: gap of 100 bp
 * 59953 74496: contrig of 14544 bp in length
 * 74497 74596: gap of 100 bp
 * 74597 74597: gap of 100 bp
 * 74597 87440: contrig of 12844 bp in length
 * 87441 87540: gap of 100 bp
 * 87541 99577: contrig of 12037 bp in length
 * 99578 99677: gap of 100 bp

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* 99678 110659: contig of 10982 bp in length
* 110660 110759: gap of 100 bp
* 110760 115413: contig of 4654 bp in length
* 115414 115513: gap of 100 bp
* 115514 124990: contig of 9477 bp in length
* 124991 125090: gap of 100 bp
* 125091 135744: contig of 10654 bp in length
* 135745 135844: gap of 100 bp
* 135845 145972: contig of 10128 bp in length
* 145973 146072: gap of 100 bp
* 146073 153170: contig of 7098 bp in length
* 153171 153270: gap of 100 bp
* 153271 156398: contig of 3128 bp in length
* 156399 156498: gap of 100 bp
* 156499 161724: contig of 5226 bp in length
* 161725 161824: gap of 100 bp
* 161825 165688: contig of 3864 bp in length
* 165689 165788: gap of 100 bp
* 165789 169698: contig of 3910 bp in length
* 169699 169798: gap of 100 bp
* 169799 173554: contig of 3756 bp in length
* 173555 173654: gap of 100 bp
* 173655 175764: contig of 2110 bp in length
* 175765 175864: gap of 100 bp
* 175865 177303: contig of 1439 bp in length
* 177304 177403: gap of 100 bp
* 177404 179097: contig of 1694 bp in length
* 179098 179197: gap of 100 bp
* 179198 181636: contig of 2439 bp in length
* 181637 181736: gap of 100 bp
* 181737 183644: contig of 1908 bp in length
* 183645 183744: gap of 100 bp
* 183745 184761: contig of 1017 bp in length
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FEATURES

source

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1. 186351
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/db xref="taxon:9606"
/chromosome="18"
/map="18q22"
/clone="RP11-879N20"
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misc_feature 74597..87440
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misc_feature 146073..153170
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Query Match 100.0%; Score 19; DB 2; Length 186351;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTGTATTCTGCTCTG 19
Db 179287 CGCTGTATTCTGCTCTG 179269

RESULT 4
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LOCUS Homo sapiens chromosome 18, clone RP11-793J2, complete sequence.
DEFINITION AC009802
AC009802.13 GI:6705901
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 191395)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckert,R., Bemm,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dekrelano,K., Depyre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
Karatas,A., Lebeckzy,J., Lieu,C., Locke,K., MacDonald,P.,
Margis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
Melgrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
Naylor,J., Niloff,M., O'Connor,I., O'Donnell,P., Pavlin,B.,
Peterson,K., Pollara,V., Riley,R., Roberts,S., Roy,A., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Tefaye,S., Tornella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
Direct Submission
Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 191395)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Bouhagalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choquet,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domano,M., Doyle,M.,
Fensterlof,D., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliier,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,U., Landers,T., Laroque,K., Lebeckzy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., MacDonald,P., Margis,N., McCarthy,M.,

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TITLE
JOURNAL
COMMENT

McGowan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J.,
Menas, L., Mihova, T., Miranda, C., Mlenka, Y., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M.,
Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A.,
Travers, M., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M.

Direct Submission
Submitted (17-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 16, 2000 this sequence version replaced gi:514043.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L1250

Center clone name: 793_J_2

FEATURES
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18843.19019
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Query Match      100.0%; Score 19; DB 9; Length 191395;
Best Local Similarity 100.0%; Fred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox 1 CGCTCGATTCGCTCTG 19
Db 97742 CGCTCGATTCGCTCTG 97760

RESULT 5
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LOCUS
DEFINITION Homo sapiens chromosome 18 clone RP11-693A18 map 18q22, WORKING
DRAFT SEQUENCE, 54 unordered pieces.
ACCESSION AF001897
VERSION AF001897.2 GI:8117548
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-693A18.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 191793)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Toroki,Y., Matanabe,H. and Sakaki,Y.
TITLE Homo sapiens 191,793 genomic DNA of 18q22
JOURNAL Published Only in Database (2000)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Toroki,Y., Matanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2000) Masahira Hattori, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
          Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
          Japan (E-mail:hattori@gsc.riken.go.jp,
          url:http://hgp-gsc.riken.go.jp/, Tel:81-42-778-9923,
          Fax:81-42-778-9924)
COMMENT On May 30, 2000 this sequence version replaced gi:7649784.

----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp-gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp

----- Project Information
Center project name: HumDrat18
Center clone name: RP11-693A18

----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 167461 bases at least Q40
Consensus quality: 174712 bases at least Q30
Consensus quality: 180769 bases at least Q20
Insert size: 186493; sum-of-contigs
Quality coverage: 4.60x in Q20 bases; sum-of-contigs

-----
NOTE: This is a 'working draft' sequence. It currently consists of
54 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

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1 10723 contig of 10723 bp in length
10824 19450 contig of 8627 bp in length
19551 28739 contig of 9189 bp in length
28840 37796 contig of 9957 bp in length
37897 45643 contig of 7747 bp in length
45744 53200 contig of 7457 bp in length
53301 59466 contig of 6166 bp in length
59567 65023 contig of 5457 bp in length
65124 71725 contig of 6602 bp in length
71826 77046 contig of 5221 bp in length
77147 82059 contig of 4913 bp in length
82160 86515 contig of 4356 bp in length
86616 90836 contig of 4221 bp in length
90937 95257 contig of 4321 bp in length
95358 99276 contig of 3919 bp in length
99377 103751 contig of 4375 bp in length
103852 108407 contig of 4556 bp in length
108508 112468 contig of 3961 bp in length
112569 116411 contig of 3843 bp in length
116512 120690 contig of 4179 bp in length
120791 125788 contig of 4999 bp in length
125890 129429 contig of 3540 bp in length
129530 132875 contig of 3346 bp in length
132976 136718 contig of 3743 bp in length
136819 140204 contig of 3386 bp in length
140305 143212 contig of 2908 bp in length
143313 146311 contig of 2999 bp in length
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153572 155905 contig of 2334 bp in length
156006 157930 contig of 1925 bp in length
158031 160335 contig of 2305 bp in length
160436 161957 contig of 1522 bp in length
162058 164115 contig of 2058 bp in length
164216 166374 contig of 2159 bp in length
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172832 174464 contig of 1633 bp in length
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177019 178822 contig of 1804 bp in length
178923 180077 contig of 1155 bp in length
180178 181248 contig of 1071 bp in length
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182600 183806 contig of 207 bp in length
182807 183992 contig of 1086 bp in length
184093 185198 contig of 1106 bp in length
185299 186320 contig of 1102 bp in length
186421 187601 contig of 1181 bp in length
187702 189099 contig of 1378 bp in length
189200 190576 contig of 1377 bp in length
190677 191793 contig of 1117 bp in length

Sequence updated (26-May-2000).
NOTE: This is a 'working draft' sequence. It currently
consists of 54 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 10723: contig of 10723 bp in length
* 10724 10823: gap of 100 bp
* 10824 19450: contig of 8627 bp in length
* 19451 19550: gap of 100 bp
* 19551 28739: contig of 9189 bp in length
* 28740 28839: gap of 100 bp
* 28840 37796: contig of 8957 bp in length
* 37797 37896: gap of 100 bp
* 37897 45643: contig of 7747 bp in length
* 45644 45743: gap of 100 bp

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45744 53200: contig of 7457 bp in length
53201 53300: gap of 100 bp
53301 59466: contig of 6166 bp in length
59467 59566: gap of 100 bp
59567 65023: contig of 5457 bp in length
65024 65123: gap of 100 bp
65124 71725: contig of 6602 bp in length
71726 71825: gap of 100 bp
71826 77046: contig of 5221 bp in length
77047 77146: gap of 100 bp
77147 82059: contig of 4913 bp in length
82060 82159: gap of 100 bp
82160 86515: contig of 4356 bp in length
86516 86615: gap of 100 bp
86616 90836: contig of 4221 bp in length
90837 90936: gap of 100 bp
90937 95257: contig of 4321 bp in length
95258 95357: gap of 100 bp
95358 99276: contig of 3919 bp in length
99277 99376: gap of 100 bp
99377 103751: contig of 4375 bp in length
103752 103851: gap of 100 bp
103852 108407: contig of 4556 bp in length
108408 108507: gap of 100 bp
108508 112468: contig of 3961 bp in length
112469 112568: gap of 100 bp
112569 116411: contig of 3843 bp in length
116412 116511: gap of 100 bp
116512 120690: contig of 4179 bp in length
120691 120790: gap of 100 bp
120791 125789: contig of 4999 bp in length
125790 125889: gap of 100 bp
125890 129429: contig of 3540 bp in length
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129530 132875: contig of 3346 bp in length
132876 132975: gap of 100 bp
132976 136718: contig of 3743 bp in length
136719 136818: gap of 100 bp
136819 140204: contig of 3386 bp in length
140205 140304: gap of 100 bp
140305 143212: contig of 2908 bp in length
143213 143312: gap of 100 bp
143313 146311: contig of 2999 bp in length
146312 146411: gap of 100 bp
146412 148694: contig of 2283 bp in length
148695 148794: gap of 100 bp
148795 151551: contig of 2757 bp in length
151552 151651: gap of 100 bp
151652 153471: contig of 1820 bp in length
153472 153571: gap of 100 bp
153572 155905: contig of 2334 bp in length
155906 156005: gap of 100 bp
156006 157930: contig of 1929 bp in length
157931 158030: gap of 100 bp
158031 160335: contig of 2305 bp in length
160336 160435: gap of 100 bp
160436 161957: contig of 1522 bp in length
161958 162057: gap of 100 bp
162058 164115: contig of 2058 bp in length
164116 164215: gap of 100 bp
164216 166374: contig of 2159 bp in length
166375 166474: gap of 100 bp
166475 168634: contig of 2160 bp in length
168635 168734: gap of 100 bp
168735 170796: contig of 2062 bp in length
170797 170896: gap of 100 bp
170897 172731: contig of 1835 bp in length
172732 172831: gap of 100 bp
172832 174464: contig of 1633 bp in length
174465 174564: gap of 100 bp
174565 175680: contig of 1116 bp in length
175681 175780: gap of 100 bp
175781 176918: contig of 1138 bp in length

```

```

Query Match      100.0%; Score 19; DB 2; Length 191793;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Ct 1 CGCTGATTCGCTCTG 19
Db 28583 CGCTGATTCGCTCTG 28565

```

```

AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

```

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.

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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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AC067875 199291 bp DNA linear HMG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589B3 map 18, *** SEQUENCING
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	* as soon as it is available and the accession number will
	* be preserved.
	* 1 38268: contig of 38268 bp in length
	* 38269 38368: gap of 100 bp
	* 38369 109704: contig of 71336 bp in length
	* 109705 109804: gap of 100 bp
	* 109805 128704: contig of 18900 bp in length
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	/chromosome="18"
	/map="18"
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	/clone_id="RP11-589E3"
BASE COUNT	62849 a 38924 c 38683 g 57534 t 301 others
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Query Match	100.0%; Score 19; DB 2; Length 198291;
Best Local Similarity	100.0%; Pred. No. 20;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGCTGTATTCGCTCTG 19
Ds	182643 CGCTGTATTCGCTCTG 182661
RESULT 7	
AC090224	AC090224 201734 bp DNA linear HTG 23-MAY-2001
LOCUS	Homo sapiens chromosome 18 clone RP11-693A18 map 18, WORKING DRAFT SEQUENCE, 8 unordered pieces.
DEFINITION	SEQUENCE, 8 unordered pieces.
ACCESSION	AC090224.4 GI:14190716
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 201734) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 18, clone RP11-693A18 Unpublished 2 (bases 1 to 201734) Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barra,N., Bartel,V., Boguski,M., Brown,A., Brown,A., Carnaroli,J., Campione,A., Choquet,Y., Collins,S., Collins,S., Cooke,P., DeRubeis,R., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Garavito,S., Ginde,S., Givner,M., Graham,L., Grand-Pierre,N., Jones,B., Keefe,A., Kohn,D., Lalonde,M., Liaw,D., Lin,X., Liu,Q., Luo,H., Maizumi,T., Makarewicz,I., McPherson,J., McPherson,R., Melnick,J., Meneses,L., Milosavljevic,A., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkung,P., Pierre,N., Pollara,V., Raymond,C., Retta,K., Rhoades,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnuppack,R., Seaman,S., Severy,P., Soumerai,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strussner,N., Subramanian,A., Talamas,J., Testeys,S., Theodore,J., Treviers,M., Travis,N., Trifunovic,J., Vasilevich,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitnov,J., Zemke,L., Zimmer,A. and Zody,M. Direct Submission
TITLE	Submitted (11-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL	On May 23, 2001 this sequence version replaced gi:13621272.
COMMENT	All repeats were identified using RepeatMasker: Smith, A.F.A. & Green, P. (1996-1997)

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http://ftp.genome.washington.edu/JM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Res
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: l12265
Center clone name: 693_A18
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 198542 bases at least Q40
Consensus quality: 200270 bases at least Q30
Consensus quality: 200829 bases at least Q20
Insert size: 194000; agarose-fp
Insert size: 201034; sum-of-contigs
Quality coverage: 11.3 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 45183: contig of 45183 bp in length
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* 45284 46768: contig of 1485 bp in length
* 46769 46868: gap of 100 bp
* 46869 47961: contig of 1093 bp in length
* 47962 48061: gap of 100 bp
* 48062 48643: contig of 1582 bp in length
* 48644 49743: gap of 100 bp
* 49744 51393: contig of 1650 bp in length
* 51394 51493: gap of 100 bp
* 51494 74531: contig of 23038 bp in length
* 74532 74631: gap of 100 bp
* 74632 127710: contig of 53079 bp in length
* 127711 127810: gap of 100 bp
* 127811 201734: contig of 73924 bp in length.
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* /chromosome="18"
* /map="18"
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* /clone_lib="RPC1-11 Human Male BAC"
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* 1. 45183
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* clone_end:SP6
* vector_side:left"
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* misc_feature
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* /note="assembly_fragment"
* 46869..47961
* /note="assembly_fragment"
* 48062..49643
* /note="assembly_fragment"
* 49744..51393
* /note="assembly_fragment"
* 51494..74531
* /note="assembly_fragment"
* 74532..127710
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* 127811..201734
* /note="assembly_fragment"
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* vector_side:right"

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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCGATTCCTGCTG 19
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 DB 147537 CGCTCGATTCCTGCTG 147555

RESULT 8
 AF140243/c 2121 bp mRNA linear VRT 07-MAR-2000
 DEFINITION Xenopus laevis axin-related protein mRNA, complete cds.
 ACCESSION AF140243
 VERSION AF140243.1 GI:6652990
 KEYWORDS
 SOURCE Xenopus laevis.
 ORGANISM Xenopus laevis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 2121)
 Itoh, K., Antipova, A., Ratcliffe, M. J. and Sokol, S.
 Interaction of dishevelled and Xenopus axin-related protein is
 required for wnt signal transduction
 Mol. Cell. Biol. 20 (6), 2228-2238 (2000)

JOURNAL MEDLINE 2013783
 PUBMED 10688669
 REFERENCE 2 (bases 1 to 2121)
 Antipova, A., Itoh, K. and Sokol, S.
 Direct Submission
 Submitted (02-APR-1999) Microbiology and Medical Genetics, Harvard
 Medical School, BIDMC, East Campus, RW663, 330 Brookline Avenue,
 Boston, MA 02215, USA
 Location/Qualifiers
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 VPDQOEIOBAMBOEAFSTFLOSDICEKRGVDEPTESPGGLPLTLEDEFG
 LHHPSGSGKINRAFSRIPRNRSHFRKTCOTQVAPASINDSEISSDILFEDSM
 SNTDSVDGIPPRSKKOREIRSVSANGKYSLPFVPRTRPAEMFSPSPRAKTI
 TIALRKVKQDAEKLKEKLQLEERLADYDISSSHVTPGALEDDOSTLID
 HVSRYLKTNPANISPRSQSPVQKGFOPASKEQTSCHLPKVPQEMETSTLAS
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 AKLMKHEHREAVTTPCEPKKATRAASOPAHPLIDTSMPLTAPNTLDLEARR
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 EVSEDAVLPFERKILCKVERAC"

BASE COUNT 637 a 501 c 507 g 476 t
 ORIGIN

Query Match 91.6%; Score 17.4; DB 5; Length 2121;
 Best Local Similarity 94.7%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCTCGATTCCTGCTG 19
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 DB 1490 CGCTCGATTCCTGCTG 1472

RESULT 9

AC127432

LOCUS AC127432 151130 bp DNA linear ROD 16-JUL-2002
 DEFINITION Mus musculus clone RP24-535L6, complete sequence.
 ACCESSION AC127432
 VERSION AC127432.1 GI:21844636
 KEYWORDS HTG.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 151130)
 McPherson, J.D. and Waterston, R.H.
 The sequence of Mus musculus clone
 Unpublished
 2 (bases 1 to 151130)
 McPherson, J.D. and Waterston, R.H.
 Direct Submission
 Submitted (16-JUL-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA

COMMENT ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: W09SC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 ----- Project Information -----
 Center project name: M BB0535L06

FEATURES
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 /db_xref="taxon:10090"
 /clone="RP24-535L6"

BASE COUNT 4308 a 3212 c 32537 g 43383 t
 ORIGIN

Query Match 91.6%; Score 17.4; DB 10; Length 151130;
 Best Local Similarity 94.7%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCTCGATTCCTGCTG 19
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 DB 99788 CGCTCGATTCCTGCTG 99806

RESULT 10
 AC128860

LOCUS AC128860 151395 bp DNA linear HTG 24-JUL-2002
 DEFINITION Rattus norvegicus clone CH230-43707, *** SEQUENCING IN PROGRESS
 ACCESSION AC128860
 VERSION AC128860.1 GI:21952979
 KEYWORDS HTG; HTGS; PHASEL.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 151395)
 Wuzny, D.M., Adams, C., Adio-Oduola, B., Ali-oshan, F.R., Allen, C.,
 Alshrook, S.L., Amarantunge, H.C., Are, J.R., Ayala, M., Banks, T.,
 Barbarta, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowie, S., Brieval, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, C., Burch, P., Burkett, C., Burrill, K.L., Byrd, N.C.,
 Carron, T.P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhury, L., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dedertich, D.A.,
 Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dink, H.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earmhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, D., Foster, P., Frantz, P.,
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* 76711 79026: contig of 2316 bp in length
* 79027 79126: gap of unknown length
* 79127 81402: contig of 2276 bp in length
* 81403 81502: gap of unknown length
* 81503 85009: contig of 3507 bp in length
* 85010 85109: gap of unknown length
* 85110 87545: contig of 2436 bp in length
* 87546 87645: gap of unknown length
* 87646 89759: contig of 2114 bp in length
* 89760 92888: gap of unknown length
* 92889 92988: contig of 3029 bp in length
* 92989 96176: gap of unknown length
* 96177 96277: gap of unknown length
* 96278 99868: contig of 3592 bp in length
* 99869 104700: gap of unknown length
* 104701 104800: gap of unknown length
* 104801 108393: contig of 3592 bp in length
* 108393 111786: gap of unknown length
* 111787 111886: contig of 3294 bp in length
* 111887 116187: gap of unknown length
* 116188 116287: gap of unknown length
* 116288 119502: contig of 3215 bp in length
* 119503 123632: gap of unknown length
* 123633 123732: contig of 4030 bp in length
* 123732: gap of unknown length

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Query Match      91.6%; Score 17.4; DB 2; Length 151395;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Cy 1 CGCTGATTCGCTGCTG 19
Db 73184 CTCTGATTCGCTG 73202

```

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RESULT 11
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LOCUS
DEFINITION
Rattus norvegicus clone CH230-22502, *** SEQUENCING IN PROGRESS
ACCESSION
AC119463
VERSION
AC119463.3 GI:21746638
KEYWORDS
HTG: HTGS PHASE1.
SOURCE
Rattus norvegicus
ORGANISM
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 168369)
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,
Alshrocks,S.L., Amaratunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonin,D.,
Boucha,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Homesi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobsen,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

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REFERENCE
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT

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Li,J., Li,Z., Lichtarge,O., Lien,C., Liu,J., Liu,W., Lounseged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawliny,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabhat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokkenwo,S., Oguth,M., Okunolu,G.,
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Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shoshitari,N., Stinson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Syatex,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tamey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Tumani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
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Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 168369)
REFERENCE
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT
Mortley,K.C.
Direct Submission
Submitted (27-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168369)
Mortley,K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20367276.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GRRZ
Center clone name: CH230-22502
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
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Consensus quality: 11142 bases at least Q30
Consensus quality: 116085 bases at least Q20
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
* consists of 74 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1052: contig of 1052 bp in length
* 1053 1152: gap of unknown length
* 1153 2488: contig of 1336 bp in length
* 2489 2589: gap of unknown length
* 2589 4101: contig of 1513 bp in length
* 4102 4201: gap of unknown length
* 4202 5283: contig of 1082 bp in length
* 5284 5383: gap of unknown length
* 5384 6393: contig of 1010 bp in length
* 6394 6493: gap of unknown length
* 6494 8259: contig of 1766 bp in length
* 8260 8359: gap of unknown length
* 8360 9702: contig of 1343 bp in length

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* 9703 9602: gap of unknown length
* 9603 1137: contig of 133 bp in length
* 1138 1137: gap of unknown length
* 1138 12257: contig of 1020 bp in length
* 12358 12357: gap of unknown length
* 12358 13355: contig of 1536 bp in length
* 13356 14055: gap of unknown length
* 14056 15337: contig of 1882 bp in length
* 15338 17706: contig of 1669 bp in length
* 17707 17806: gap of unknown length
* 17807 19352: contig of 1546 bp in length
* 19353 19452: gap of unknown length
* 19453 20883: contig of 1431 bp in length
* 20884 20983: gap of unknown length
* 20984 22048: contig of 1065 bp in length
* 22049-22148: gap of unknown length
* 22149 23896: contig of 1748 bp in length
* 23897 23996: gap of unknown length
* 23997 25356: contig of 1360 bp in length
* 25357 26764: gap of unknown length
* 26765 26864: gap of unknown length
* 26865 27982: contig of 1118 bp in length
* 27983 28082: gap of unknown length
* 28083 29140: contig of 1058 bp in length
* 29141 29240: gap of unknown length
* 29241 30671: contig of 1431 bp in length
* 30672 30772: gap of unknown length
* 30772 32820: contig of 2049 bp in length
* 32821 32920: gap of unknown length
* 32921 34405: contig of 1485 bp in length
* 34406 34505: gap of unknown length
* 34506 36497: contig of 1992 bp in length
* 36498 36597: gap of unknown length
* 36598 37336: contig of 1033 bp in length
* 37337 37736: gap of unknown length
* 37737 39316: contig of 1580 bp in length
* 39317 39416: gap of unknown length
* 39417 40439: contig of 1023 bp in length
* 40440 40539: gap of unknown length
* 40540 41568: contig of 1025 bp in length
* 41569 41668: gap of unknown length
* 41669 42719: contig of 1051 bp in length
* 42720 42819: gap of unknown length
* 42820 44594: contig of 1775 bp in length
* 44595 44694: gap of unknown length
* 44695 45911: contig of 1217 bp in length
* 45912 46011: gap of unknown length
* 46012 47510: contig of 1499 bp in length
* 47511 47610: gap of unknown length
* 47611 48721: contig of 1111 bp in length
* 48722 48821: gap of unknown length
* 48822 50922: contig of 2101 bp in length
* 50923 51022: gap of unknown length
* 51023 52233: contig of 1211 bp in length
* 52234 52333: gap of unknown length
* 52334 54084: contig of 1751 bp in length
* 54085 54184: gap of unknown length
* 54185 55537: contig of 1353 bp in length
* 55538 55637: gap of unknown length
* 55638 57248: contig of 1611 bp in length
* 57249 57348: gap of unknown length
* 57349 59510: contig of 2162 bp in length
* 59511 59610: gap of unknown length
* 59611 60612: contig of 1002 bp in length
* 60613 60712: gap of unknown length
* 60713 62445: contig of 1733 bp in length
* 62446 62545: gap of unknown length
* 62546 64053: contig of 1508 bp in length
* 64054 64153: gap of unknown length
* 64154 66613: contig of 2460 bp in length
* 66614 66713: gap of unknown length

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* 66714 66864: contig of 1951 bp in length
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* 70130 70229: gap of unknown length
* 70230 72519: contig of 2290 bp in length
* 72520 72619: gap of unknown length
* 72620 74651: contig of 2032 bp in length
* 74652 74751: gap of unknown length
* 74752 76057: contig of 1306 bp in length
* 76058 76157: gap of unknown length
* 76158 78182: contig of 2025 bp in length
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* 78283 79881: contig of 1599 bp in length
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* 82072 82171: contig of 2090 bp in length
* 82172 83559: gap of unknown length
* 83560 83659: contig of 1388 bp in length
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* 85036 85135: contig of 1376 bp in length
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* 87276: contig of 2141 bp in length

Query Match 91.6%; Score 17.4; DB 2; Length 168369;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGCTCGATCTCGCTG 19
Db 4044 CGCTCGATCTCGCTG 4026

RESULT 12
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DEFINITION
ACCESSION AC022377.2 GI:10305054
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 176054)
AUTHORS Lin, W., Zhang, C., Dong, H., Wan, M., Xu, S., Gu, W., Tu, Y., Jia, J.,
Wu, C., Lu, G., Zhong, M., Zhou, Y., Ren, S., Fu, G., Chen, Z. and
Huang, M.
Direct Submission
Submitted (03-FEB-2000) Genomic Dept., Chinese National Human
Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai,
Shanghai 201203, P. R. China
On Sep 26, 2000 this sequence version replaced gi:1682623.
COMMENT
-----Genome Center-----
Center: Beijing Center
Center code: Beijing
Website: http://hgsc.igtp.ac.cn
http://www.genomics.org.cn
Contact: hgsc@igtp.ac.cn.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 8523: contig of 8523 bp in length
* 8524 21709: contig of 13186 bp in length
* 21710 39761: contig of 18052 bp in length
* 39762 42545: contig of 2784 bp in length

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* * *
 * 42546 96169: contig of 53624 bp in length
 * * gap of unknown length
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 DEFINITION
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 SOURCE
 Homo sapiens
 Homo sapiens
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 1 (bases 1 to 178548)
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 AUTHORS
 Li F., Bao J., Bao Q., Bao W., Bian X., Cao T., Chen C., Chen J.,
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 Guo Z., He L., Hu S., Huang F., Jin Y., Kang N., Li C., Li C.,
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 Wang Y., Wu D., Wu Q., Xie F., Xuan Z., Xue Y., Yan C., Yang X.,
 Yu B., Zeng Y., Zhang G., Zhang H., Zhang H., Zhang L., Zhang M.,
 Zhang X., Zhang X., Zhang Y., Zhang Y., Zhang Z., Zhu B., Zhu N.,
 Yu J. and Yang H.
 TITLE
 Chromosome 3p genomic sequence
 JOURNAL
 Unpublished
 REFERENCE
 AUTHORS
 2 (bases 1 to 178548)
 Zeng Y., Hu S., Dong W., Wang J., Zhang Y., Zhang H., Liu B.,
 Bao W., Sun Y., Wu Q., Wang X., Cheng C., Wang Y., Niu Y.,
 Qi X., Li T., Zhang H., Liu N., Wu D., Yu B., Fan H., Liu Y.,
 Li G., Li C., Bao Q., Bao J., Wang J., Song L., Zhang L., Guo D.,
 Huang F., Zhang G., Li J., Bian X., Zhang M., Li L., Feng X.,
 Wang X., Yu J. and Yang H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (21-DEC-1999) Human Genomic Center, Institute of
 Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
 100101, P.R.China
 REFERENCE
 AUTHORS
 3 (bases 1 to 178548)
 Li F., Bao J., Bao Q., Bao W., Bian X., Cao T., Chen C., Chen J.,
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 Zhang X., Zhang X., Zhang Y., Zhang Y., Zhang Z., Zhu B., Zhu N.,
 Yu J. and Yang H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (09-FEB-2001) Human Genomic Center, Institute of

Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
 100101, P.R.China
 On Feb 9, 2001 this sequence version replaced gi:16862651.
 COMMENT
 -----Genome Center
 Center:Beijing Center
 Center code:Beijing
 Website:http://hgsc.igmp.ac.cn
 http://www.genomics.org.cn
 Contact:hgsc@igmp.ac.cn
 Project Information
 Center project name:18 project
 Center clone name: RP11-481B18
 ----- Summary Statistics
 Sequencing vector: pUC18; 100% of reads
 Chemistry: Dye-terminator; RT 55% of reads
 Chemistry: Dye-terminator Big Dye; 45% of reads
 Assembly program: Phrap; version 0.950329
 Consensus quality: 182029 bases at least Q40
 Consensus quality: 182113 bases at least Q30
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 Insert size: 178548; sum-of-contigs
 Quality coverage: 15.40x in Q20 bases;sum-of-contigs

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 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGCTCGATTCCTGCTCG 19
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 ***; 58 unordered pieces.
 AC125748
 AC125748.2 GI:21671833
 VERSION
 HTG; HTGS PHASE1.
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 Norway rat.
 SOURCE
 Rattus norvegicus
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 189040)
 REFERENCE
 AUTHORS
 Muzny D.M., Adams C., Adio-Ogunla B., Ali-Osman F.R., Allen C.,
 Albrooks S.L., Amaralung H.C., Are J.R., Ayale M., Banks T.,
 Barbarella J., Benson J., Biraghe K., Blankenburg K., Bonnin D.,
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 Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
 Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H.,
 Doulatwalte K.J., Diaper H., Dugan-Rocha S., Durbin K.J.,
 Barnhart C., Edgar D., Edwards C.C., Elhaj C., Escoto M.,
 Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Prantiz P.,
 Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R.,
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 Hernandez O., Hodgson A., Hogue M., Holloway C., Hollins B.,

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ORIGIN

Query Match 91.6%; Score 17.4; DB 2; Length 192180;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGCTCGATTCCTGCTCTG 19
|||||
Db 27976 CGCTCGATTCCTGCTCTG 27994

Search completed: June 21, 2003, 19:56:22
Job time : 997 secs